A UNIQUE TEXTBOOK FOR TEACHING COURSES IN BIOINFORMATICS

By Robert G. Gregerson and Tim H. Lindblom


Take a look around for textbooks explaining the foundations of bioinformatics to advanced undergraduates, and you’ll find a very limited selection. Luckily, at least one textbook fills the niche nicely and provides an excellent launching pad for undergraduates ready to begin using in silico and high-throughput biology.

Now in its second edition, Discovering Genomics, Proteomics, and Bioinformatics by A. Malcolm Campbell and Laurie J. Heyer offers a biology-centered, problem-solving approach to tackling this growing and rapidly evolving discipline. We’ve used this textbook in independent upper-level bioinformatics courses offered to undergraduates and found that its unique style makes it a very useful teaching tool.

As high-throughput and large-format approaches to biological investigation have revolutionized modern biology, many undergraduate educators have struggled to keep pace with new technological advances. In fact, it’s impractical, if not impossible, to teach the whole of bioinformatics in a single semester. Campbell and Heyer have thus wisely placed the text’s focus on the foundations of bioinformatics and the use of advanced bioinformatics tools to solve real biological problems. More of a workbook than a traditional textbook, the text very effectively guides readers through an exploration of large data sets and public databases using well-organized explanatory text, discovery questions, and case studies.

The authors put problem solving center stage in the opening chapter by using muscular dystrophy as an example to draw readers into the material and think scientifically. Almost immediately, readers are directed to public databases and bioinformatics tools to learn about this terrible disease. The themes presented here return throughout the book: many human diseases are very complex in nature, and to fully understand them requires using the new methods of genomics, proteomics, and bioinformatics. With the first chapter under their belt, readers are then primed to learn and appreciate these powerful approaches to biological problem solving. Campbell and Heyer present genomics as a way to understand biological questions and applications such as genetic variation and evolution, aging, disease pathology, pathogen population dynamics, and biowarfare.

The book’s second unit deals with gene expression on a genomic scale. As with the genomics unit, this unit opens with a case study of the biologically complex topic of human obesity. This unit is filled with biological questions that lead readers through the use of microarrays, proteomics, protein interaction networks, and protein structure prediction. Data sources to answer these questions come from the primary literature, providing an authentic experience for students. Embedded within the entire book, but used most effectively here, are links to online animations that help students follow the often complex techniques and procedures.

The third unit takes a whole genome perspective and integrates concepts from the first two units. Sticking to the biological application theme, the first chapter is a case study on drug discovery and drug–genome interactions. Subsequent chapters then illustrate genomic circuitry, beginning with the expression of a single gene up to complex genomic circuits. The final chapters cover synthetic biology and modeling biology with systematics. These later chapters exponentially increase in complexity so their inclusion might be an unrealistic goal in a single-semester undergraduate course. In our courses, we were only able to adequately cover the first two chapters, but advanced bioinformatics undergraduates and graduate students might find the complexity of genomic circuitry a challenging and worthwhile topic.
Any book that attempts to comprehensively cover this field is doomed to failure. The authors have wisely avoided that approach and have succeeded in their effort to introduce students to the kind of thinking required for the genomics, proteomics, and bioinformatics fields. The authors use Web-based resources to guide readers through each subject. This highly effective learning method places students at computers during the class period, with the instructor acting as a guide or organizer. Students leave class with an introduction to a particular topic and continue to work on “discovery questions” outside of class. The only drawback to relying on external Web sites for content delivery is that the links can change or become inactive.

This book contains much more than descriptions of techniques; they’re explained thoroughly so that readers understand why they represent the best way to investigate many complex biological questions. The only potential problem with the book’s content is that the final unit is a bit complex and difficult to connect to the preceding material. In addition, a book covering these topics requires frequent updating because of the breakneck speed of technological progress in these fields.

The writing throughout the book is very informal, which is likely to appeal to newcomers. The authors have done a good job interspersing difficult, highly detailed topics with less rigorous, more fun, and thought-provoking material. In most instances, the use of informal language is effective and welcome. Our students felt that some of the “softer” writing was too cute and occasionally distracted from the discussion. Overall, however, the case study approach is an important and welcome part of the book’s organization, enticing readers to continue through the remainder of each unit.

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